

## RAW SEQUENCE LISTING

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Application Serial Number: US/10/826,572

Source: FFWO

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/826,572

DATE: 11/18/2004

TIME: 09:28:46

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Output Set: N:\CRF4\11182004\J826572.raw

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3 <110> APPLICANT: APARICIO, SAMUEL
4   CARLTON, MARK
5   MITCHELL, PHILIP
7 <120> TITLE OF INVENTION: RECEPTOR
9 <130> FILE REFERENCE: 674580-2008
11 <140> CURRENT APPLICATION NUMBER: 10/826,572
12 <141> CURRENT FILING DATE: 2004-04-16
14 <150> PRIOR APPLICATION NUMBER: PCT/GB02/04725
15 <151> PRIOR FILING DATE: 2002-10-21
17 <150> PRIOR APPLICATION NUMBER: US 60/346,083
18 <151> PRIOR FILING DATE: 2001-10-24
20 <150> PRIOR APPLICATION NUMBER: GB 0125183.4
21 <151> PRIOR FILING DATE: 2001-10-19
23 <160> NUMBER OF SEQ ID NOS: 40
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27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1197
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
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35 accgcgaaca ttttttggtc actgagatcg agtctcccag tgctttggct tcccgcctct 180
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40 aagctggccc tcgtgctcac cggcgtgctc atcttcgccc tggcgctctt tggcaatgct 480
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55 <210> SEQ ID NO: 2
56 <211> LENGTH: 774
57 <212> TYPE: DNA

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58 &lt;213&gt; ORGANISM: Homo sapiens

60 &lt;400&gt; SEQUENCE: 2

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63 ccgggacgcg ccaagctggc cctcgtgctc accggcgtgc tcattctcgc cctggcgctc 180
64 ttggcaatg ctctgggtgt ctacgtgggtg acccgagca aggccatgcg caccgtcacc 240
65 aacatcttta tctgctcctt ggcgctcagt gacctgctca tcaccttctt ctgcattccc 300
66 gtcaccatgc tccagaacat ttccgacaac tggctggggg tgctttcat ttgcaagatg 360
67 gtgccatttg tccagtctac cgctgttggtg acagaaatcc tcactatgac ctgcattgct 420
68 gtggaaaggc accagggact tgtgcatect tttaaaatga agtggcaata caccaaccga 480
69 agggctttca caatgctagg tgtggctctgg ctgggtggcag tcactgtagg atcacccatg 540
70 tggcagctgc aacaacttga gatcaaatat gacttctat atgaaaagga acacatctgc 600
71 tgcttagaag agtggaccag cctgtgtcac cagaagatct acaccacctt catccttgct 660
72 atcctcttcc tcttgctctt tatggaagaa gaaacgagct gtcattatga tggtagacagt 720
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76 &lt;210&gt; SEQ ID NO: 3

77 &lt;211&gt; LENGTH: 258

78 &lt;212&gt; TYPE: PRT

79 &lt;213&gt; ORGANISM: Homo sapiens

81 &lt;400&gt; SEQUENCE: 3

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82 Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg
83   1           5           10           15
85 Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg
86           20           25           30
88 Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu
89           35           40           45
91 Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
92           50           55           60
94 Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
95  65           70           75           80
97 Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe
98           85           90           95
100 Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu
101           100          105          110
103 Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala
104           115          120          125
106 Val Val Thr Glu Ile Leu Thr Met Thr Cys Ile Ala Val Glu Arg His
107           130          135          140
109 Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg
110 145          150          155          160
112 Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val
113           165          170          175
115 Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe
116           180          185          190
118 Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro
119           195          200          205
121 Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu
122           210          215          220
124 Leu Pro Leu Met Glu Glu Glu Thr Ser Cys His Tyr Asp Gly Asp Ser

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125 225          230          235          240
127 Gly Gly Ser Leu Cys Val Leu Gly Thr Ile Pro Cys Cys Pro Tyr
128          245          250          255
130 Asp Asp
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135 <211> LENGTH: 774
136 <212> TYPE: DNA
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139 <400> SEQUENCE: 4
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141 actcgggaac agttcattca tcgctatggg ctgcgaccgc tgggtctacac tccggagctg 120
142 cccgcgcgcg ctaaactggc ctttgcgctg gctggagcac tcatttttgc cctggcgctc 180
143 tttggcaact ctctggtcat ctatgtggtg acccgagca aggccatgcg caccgtcacc 240
144 aacatcttca tctgctctct ggcactcagt gatctgctca ttgccttctt ctgcatcccc 300
145 gtcacgatgc tccagaacat ctccgacaag tggctgggtg gtgccttcat ctgcaagatg 360
146 gtgcccttcg tccagtcac tgctgttggt acggaaatcc tcacatgac ttgcatcgct 420
147 gttgagaggg accaaggact catccatcct tttaaaatga agtggcagta cactacccca 480
148 agggctttca caatcttggg tgtggtctgg ttggcagcca tcacgtagg atcaccatg 540
149 tggcacgtac aacgcctcga gattaagtat gacttcctct atgagaaaga acatgtctgc 600
150 tgtttgaag agtgggcccag ccccatgcac cagagaatct acaccacctt catcctcgctc 660
151 atcctcttcc tctgcccgt tgtggaagaa gaagcgggct gtcgttatga tggtgacagt 720
152 ggtggtctct ttcgtgctg gctgggcacc tttccatgtt gttcacatga tgggt 774
155 <210> SEQ ID NO: 5
156 <211> LENGTH: 258
157 <212> TYPE: PRT
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160 <400> SEQUENCE: 5
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162 1 5 10 15
164 Ala His Asn Leu Thr Arg Glu Gln Phe Ile His Arg Tyr Gly Leu Arg
165 20 25 30
167 Pro Leu Val Tyr Thr Pro Glu Leu Pro Ala Arg Ala Lys Leu Ala Phe
168 35 40 45
170 Ala Leu Ala Gly Ala Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ser
171 50 55 60
173 Leu Val Ile Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
174 65 70 75 80
176 Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Ala Phe
177 85 90 95
179 Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Lys Trp Leu
180 100 105 110
182 Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala
183 115 120 125
185 Val Val Thr Glu Ile Leu Thr Met Thr Cys Ile Ala Val Glu Arg His
186 130 135 140
188 Gln Gly Leu Ile His Pro Phe Lys Met Lys Trp Gln Tyr Thr Thr Arg
189 145 150 155 160
191 Arg Ala Phe Thr Ile Leu Gly Val Val Trp Leu Ala Ala Ile Ile Val
192 165 170 175

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194 Gly Ser Pro Met Trp His Val Gln Arg Leu Glu Ile Lys Tyr Asp Phe
195             180             185             190
197 Leu Tyr Glu Lys Glu His Val Cys Cys Leu Glu Glu Trp Ala Ser Pro
198             195             200             205
200 Met His Gln Arg Ile Tyr Thr Phe Ile Leu Val Ile Leu Phe Leu
201             210             215             220
203 Leu Pro Leu Val Glu Glu Ala Gly Cys Arg Tyr Asp Gly Asp Ser
204 225             230             235             240
206 Gly Gly Ser Leu Arg Cys Val Leu Gly Thr Phe Pro Cys Cys Ser His
207             245             250             255
209 Asp Gly

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213 &lt;210&gt; SEQ ID NO: 6

214 &lt;211&gt; LENGTH: 853

215 &lt;212&gt; TYPE: DNA

216 &lt;213&gt; ORGANISM: Mus musculus

218 &lt;400&gt; SEQUENCE: 6

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220 ctgcgcacag catgcaggcg ctcaacatca ccgcggagca gttttcccg ctgctgagcg 120
221 cgcacaacct gactcgggaa cagttcattc atcgctatgg gctgcgaccg ctggtctaca 180
222 ctccggagct gcccgcgcg ctaaaactgg cctttgcgct ggctggagca ctcatTTTTg 240
223 ccttggcgct ctttggcaac tctctggtca tctatgtggt gaccgcgagc aaggccatgc 300
224 gcaccgtcac caacatcttc atctgctctc tggcactcag tgatctgctc attgccttct 360
225 tctgcatccc cgtcacgatg ctccagaaca tctccgacaa gtggctgggt ggtgccttca 420
226 tctgcaagat ggtgcccttc gtccagtcca ctgctgttgt gacggaaatc ctaccatga 480
227 cttgcatcgc tgttgagagg caccaaggac tcatccatcc ttttaaaatg aagtggcagt 540
228 aactaccg aagggtcttc acaatcttgg gtgtggtctg gttggcagcc atcatcgtag 600
229 gatcacccat gtggcacgta caacgcctcg agattaagta tgacttcctc tatgagaaag 660
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236 &lt;210&gt; SEQ ID NO: 7

237 &lt;211&gt; LENGTH: 1791

238 &lt;212&gt; TYPE: DNA

239 &lt;213&gt; ORGANISM: Homo sapiens

241 &lt;400&gt; SEQUENCE: 7

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243 gcaccccgaga ccgtggcggc gcctcgctt aggggaagagc aagggaagaa ctttatttga 120
244 accgcgaaca ttttttggtc actgagatcg agtctccag tcttttggt tcccgcctct 180
245 ttatcgtggg tttgatccct gagctgctct cctttccctc gctgcccgc agatgcggat 240
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247 aacattaccc cggagcagtt ctctcggtg ctgcgggacc acaacctgac gcgggagcag 360
248 ttcatcgctc tgtaccggt gcgaccgctc gtctacaccc cagagctgcc gggacgcgcc 420
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252 cagaacattt ccgacaactg gctggggggg gctttcattt gcaagatggt gccatttgct 660
253 cagtctaccg ctgttgtgac agaaatctc actatgacct gcattgctgt ggaaaggcac 720
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257 tggaccagcc ctgtgcacca gaagatctac accaccttca tccttgatcat cctcttctc 960
258 ctgcctctta tgggtgatgct tattctgtac agtaaaattg gttatgaact ttggataaag 1020
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274 &lt;210&gt; SEQ ID NO: 8

275 &lt;211&gt; LENGTH: 1293

276 &lt;212&gt; TYPE: DNA

277 &lt;213&gt; ORGANISM: Homo sapiens

279 &lt;400&gt; SEQUENCE: 8

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281 acgcgggagc agttcatcgc tctgtaccgg ctgcgaccgc tcgtctacac cccagagctg 120
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306 &lt;212&gt; TYPE: PRT

307 &lt;213&gt; ORGANISM: Homo sapiens

309 &lt;400&gt; SEQUENCE: 9

VERIFICATION SUMMARY

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